

WO 2004/042059

SEQUENCE LISTING

<110> The University of Queensland (all states, except U.S.)  
 Frazer, Ian Hector (U.S. only)

<120> A method for optimising gene expression

<130> 12178192/VPA

<140> Unassigned

<141> 2003-11-10

<150> USSN 60/425,163

<151> 2002-11-08

<160> 126

<170> PatentIn version 3.2

<210> 1

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised GFP

<220>

<221> CDS

<222> (1)..(711)

<400> 1

agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	gtc	cca	att	ctc	gtg	gaa	48
Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	
1				5					10					15		
ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	tct	gtc	agc	gga	gag	ggc	96
Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	
			20					25					30			
gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	ctg	aaa	ttc	atc	tgc	acc	144
Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	
			35					40					45			
act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	ctg	gtc	act	acc	ttc	tct	192
Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Ser	
	50					55					60					
tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	gac	cat	atg	aag	cag	cat	240
Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	
65					70					75				80		
gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	tat	gtg	cag	gag	aga	acc	288
Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	
				85					90					95		
atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	acc	cgc	gct	gaa	gtc	aag	336
Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	
			100					105					110			
ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	gag	ctg	aag	ggc	att	gac	384

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp  
 115 120 125

ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat 432  
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr  
 130 135 140

aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc 480  
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile  
 145 150 155 160

aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag 528  
 Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln  
 165 170 175

ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg 576  
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val  
 180 185 190

ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa 624  
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys  
 195 200 205

gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc 672  
 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr  
 210 215 220

gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 714  
 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

<210> 2  
 <211> 237  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Humanised GFP

<400> 2

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu  
 1 5 10 15

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly  
 20 25 30

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr  
 35 40 45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser  
 50 55 60

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His  
 65 70 75 80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr  
85 90 95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys  
100 105 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp  
115 120 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr  
130 135 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile  
145 150 155 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln  
165 170 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val  
180 185 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys  
195 200 205

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr  
210 215 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
225 230 235

<210> 3

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ala(GCA)x6

<220>

<221> CDS

<222> (1)..(18)

<400> 3

gca gca gca gca gca gca  
Ala Ala Ala Ala Ala Ala  
1 5

18

<210> 4

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Ala (GCA) x6

<400> 4

Ala Ala Ala Ala Ala Ala

1

5

<210> 5

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ala (GCG) x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 5

gcg gcg gcg gcg gcg gcg

Ala Ala Ala Ala Ala Ala

1

5

18

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Ala (GCG) x6

<400> 6

Ala Ala Ala Ala Ala Ala

1

5

<210> 7

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ala (GCT) x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 7

gct gct gct gct gct gct

Ala Ala Ala Ala Ala Ala

1

5

18

<210> 8  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ala (GCT) x6

<400> 8

Ala Ala Ala Ala Ala Ala  
1 5

<210> 9  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ala (GCC) x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 9  
gcc gcc gcc gcc gcc gcc  
Ala Ala Ala Ala Ala Ala  
1 5

18

<210> 10  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ala (GCC) x6

<400> 10

Ala Ala Ala Ala Ala Ala  
1 5

<210> 11  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Arg (AGA) x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 11

aga aga aga aga aga aga  
Arg Arg Arg Arg Arg Arg  
1 5

18

<210> 12  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Arg(AGA)x6

<400> 12

Arg Arg Arg Arg Arg Arg  
1 5

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Arg(CGA)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 13  
cga cga cga cga cga cga  
Arg Arg Arg Arg Arg Arg  
1 5

18

<210> 14  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Arg(CGA)x6

<400> 14

Arg Arg Arg Arg Arg Arg  
1 5

<210> 15  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Arg(CGG)x6

<220>

<221> CDS  
<222> (1) .. (18)

<400> 15  
cgg cgg cgg cgg cgg cgg  
Arg Arg Arg Arg Arg Arg  
1 5

18

<210> 16  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Arg(CGG)x6

<400> 16

Arg Arg Arg Arg Arg Arg  
1 5

<210> 17  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Arg(CGT)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 17  
cgt cgt cgt cgt cgt cgt  
Arg Arg Arg Arg Arg Arg  
1 5

18

<210> 18  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Arg(CGT)x6

<400> 18

Arg Arg Arg Arg Arg Arg  
1 5

<210> 19  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Arg (AGG) x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 19

agg agg agg agg agg agg

Arg Arg Arg Arg Arg Arg

1 5

18

<210> 20

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Arg (AGG) x6

<400> 20

Arg Arg Arg Arg Arg Arg

1 5

<210> 21

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Arg (CGC) x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 21

cgc cgc cgc cgc cgc cgc

Arg Arg Arg Arg Arg Arg

1 5

18

<210> 22

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Arg (CGC) x6

<400> 22

Arg Arg Arg Arg Arg Arg

1 5

<210> 23

<211> 18



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Asn(AAC)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 23  
aac aac aac aac aac aac  
Asn Asn Asn Asn Asn Asn  
1 5

18

<210> 24  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Asn(AAC)x6

<400> 24

Asn Asn Asn Asn Asn Asn  
1 5

<210> 25  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Asn(AAT)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 25  
aat aat aat aat aat aat  
Asn Asn Asn Asn Asn Asn  
1 5

18

<210> 26  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Asn(AAT)x6

<400> 26

Asn Asn Asn Asn Asn Asn  
1 5

<210> 27  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Asp (GAT) x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 27  
gat gat gat gat gat gat  
Asp Asp Asp Asp Asp Asp  
1 5

18

<210> 28  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Asp (GAT) x6

<400> 28

Asp Asp Asp Asp Asp Asp  
1 5

<210> 29  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Asp (GAC) x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 29  
gac gac gac gac gac gac  
Asp Asp Asp Asp Asp Asp  
1 5

18

<210> 30  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Asp (GAC) x6

<400> 30

Asp Asp Asp Asp Asp Asp  
1 5

<210> 31

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Cys (TGC)x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 31

tgc tgc tgc tgc tgc tgc  
Cys Cys Cys Cys Cys Cys  
1 5

18

<210> 32

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Cys (TGC)x6

<400> 32

Cys Cys Cys Cys Cys Cys  
1 5

<210> 33

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Cys (TGT)x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 33

tgt tgt tgt tgt tgt tgt  
Cys Cys Cys Cys Cys Cys  
1 5

18

<210> 34

<211> 6

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Cys (TGT) x6

&lt;400&gt; 34

Cys Cys Cys Cys Cys Cys  
1 5

&lt;210&gt; 35

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Gln(CAA) x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (18)

&lt;400&gt; 35

caa caa caa caa caa caa  
Gln Gln Gln Gln Gln Gln  
1 5

18

&lt;210&gt; 36

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Gln(CAA) x6

&lt;400&gt; 36

Gln Gln Gln Gln Gln Gln  
1 5

&lt;210&gt; 37

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Gln(CAG) x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (18)

&lt;400&gt; 37

cag cag cag cag cag cag  
Gln Gln Gln Gln Gln Gln  
1 5

18

<210> 38  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gln(CAG)x6

<400> 38

Gln Gln Gln Gln Gln Gln  
1 5

<210> 39  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Glu(GAA)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 39  
gaa gaa gaa gaa gaa gaa  
Glu Glu Glu Glu Glu Glu  
1 5

18

<210> 40  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Glu(GAA)x6

<400> 40

Glu Glu Glu Glu Glu Glu  
1 5

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Glu(GAG)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 41  
gag gag gag gag gag gag

18

Glu Glu Glu Glu Glu Glu  
1 5

<210> 42  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Glu(GAG)x6

<400> 42

Glu Glu Glu Glu Glu Glu  
1 5

<210> 43  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Gly(GGA)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 43  
gga gga gga gga gga gga  
Gly Gly Gly Gly Gly Gly  
1 5

18

<210> 44  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gly(GGA)x6

<400> 44

Gly Gly Gly Gly Gly Gly  
1 5

<210> 45  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Gly(GGG)x6

<220>  
<221> CDS

<222> (1) .. (18)

<400> 45

ggg ggg ggg ggg ggg ggg  
Gly Gly Gly Gly Gly Gly  
1 5

18

<210> 46

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Gly(GGG)x6

<400> 46

Gly Gly Gly Gly Gly Gly  
1 5

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Gly(GGC)x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 47

ggc ggc ggc ggc ggc ggc  
Gly Gly Gly Gly Gly Gly  
1 5

18

<210> 48

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Gly(GGC)x6

<400> 48

Gly Gly Gly Gly Gly Gly  
1 5

<210> 49

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Gly(GGT)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 49  
ggt ggt ggt ggt ggt ggt  
Gly Gly Gly Gly Gly Gly  
1 5

18

<210> 50  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gly (GGT) x6

<400> 50  
Gly Gly Gly Gly Gly Gly  
1 5

<210> 51  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> His (CAC) x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 51  
cac cac cac cac cac cac  
His His His His His His  
1 5

18

<210> 52  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> His (CAC) x6

<400> 52  
His His His His His His  
1 5

<210> 53  
<211> 18  
<212> DNA



<213> Artificial Sequence

<220>

<223> His (CAT)x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 53

cat cat cat cat cat cat

18

His His His His His His

1

5

<210> 54

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> His (CAT)x6

<400> 54

His His His His His His

1

5

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ile (ATC)x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 55

atc atc atc atc atc atc

18

Ile Ile Ile Ile Ile Ile

1

5

<210> 56

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Ile (ATC)x6

<400> 56

Ile Ile Ile Ile Ile Ile

1

5

<210> 57  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ile(ATT)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 57  
att att att att att att  
Ile Ile Ile Ile Ile Ile  
1 5

18

<210> 58  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ile(ATT)x6

<400> 58

Ile Ile Ile Ile Ile Ile  
1 5

<210> 59  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ile(ATA)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 59  
ata ata ata ata ata ata  
Ile Ile Ile Ile Ile Ile  
1 5

18

<210> 60  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ile(ATA)x6

<400> 60

Ile Ile Ile Ile Ile Ile  
1 5

<210> 61  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Leu(CTC)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 61  
ctc ctc ctc ctc ctc ctc  
Leu Leu Leu Leu Leu Leu  
1 5

18

<210> 62  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Leu(CTC)x6

<400> 62

Leu Leu Leu Leu Leu Leu  
1 5

<210> 63  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Leu(TTG)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 63  
ttg ttg ttg ttg ttg ttg  
Leu Leu Leu Leu Leu Leu  
1 5

18

<210> 64  
<211> 6  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Leu(TTG)x6

&lt;400&gt; 64

Leu Leu Leu Leu Leu Leu

1

5

&lt;210&gt; 65

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Leu(CTA)x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(18)

&lt;400&gt; 65

cta cta cta cta cta cta

18

Leu Leu Leu Leu Leu Leu

1

5

&lt;210&gt; 66

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Leu(CTA)x6

&lt;400&gt; 66

Leu Leu Leu Leu Leu Leu

1

5

&lt;210&gt; 67

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Leu(CTG)x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(18)

&lt;400&gt; 67

ctg ctg ctg ctg ctg ctg

18

Leu Leu Leu Leu Leu Leu

1

5

&lt;210&gt; 68

<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Leu(CTG)x6

<400> 68

Leu Leu Leu Leu Leu Leu  
1 5

<210> 69  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Leu(TTA)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 69  
tta tta tta tta tta tta  
Leu Leu Leu Leu Leu Leu  
1 5

18

<210> 70  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Leu(TTA)x6

<400> 70

Leu Leu Leu Leu Leu Leu  
1 5

<210> 71  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Leu(CTT)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 71  
ctt ctt ctt ctt ctt ctt  
Leu Leu Leu Leu Leu Leu

18

1 5

<210> 72  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Leu(CTT)x6

<400> 72

Leu Leu Leu Leu Leu Leu  
1 5

<210> 73  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Lys(AAG)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 73  
aag aag aag aag aag aag  
Lys Lys Lys Lys Lys Lys  
1 5

18

<210> 74  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Lys(AAG)x6

<400> 74

Lys Lys Lys Lys Lys Lys  
1 5

<210> 75  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Lys(AAA)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 75  
aaa aaa aaa aaa aaa aaa  
Lys Lys Lys Lys Lys Lys  
1 5 18

<210> 76  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Lys (AAA)x6

<400> 76  
Lys Lys Lys Lys Lys Lys  
1 5

<210> 77  
<211> 18  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Phe (TTT)x6

<220>  
<221> CDS  
<222> (1) .. (18)

<400> 77  
ttt ttt ttt ttt ttt ttt  
Phe Phe Phe Phe Phe Phe  
1 5 18

<210> 78  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Phe (TTT)x6

<400> 78  
Phe Phe Phe Phe Phe Phe  
1 5

<210> 79  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Phe (TTC)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 79  
ttc ttc ttc ttc ttc ttc  
Phe Phe Phe Phe Phe Phe  
1 5

18

<210> 80  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Phe(TTC)x6

<400> 80

Phe Phe Phe Phe Phe Phe  
1 5

<210> 81  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Pro(CCC)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 81  
ccc ccc ccc ccc ccc ccc  
Pro Pro Pro Pro Pro Pro  
1 5

18

<210> 82  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Pro(CCC)x6

<400> 82

Pro Pro Pro Pro Pro Pro  
1 5

<210> 83  
<211> 18  
<212> DNA  
<213> Artificial Sequence



&lt;220&gt;

&lt;223&gt; Pro (CCT) x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (18)

&lt;400&gt; 83

cct cct cct cct cct cct

18

Pro Pro Pro Pro Pro Pro

1

5

&lt;210&gt; 84

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Pro (CCT) x6

&lt;400&gt; 84

Pro Pro Pro Pro Pro Pro

1

5

&lt;210&gt; 85

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Pro (CCG) x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (18)

&lt;400&gt; 85

ccg ccg ccg ccg ccg ccg

18

Pro Pro Pro Pro Pro Pro

1

5

&lt;210&gt; 86

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Pro (CCG) x6

&lt;400&gt; 86

Pro Pro Pro Pro Pro Pro

1

5

<210> 87  
 <211> 18  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Pro(CCA)x6

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 87  
 cca cca cca cca cca cca  
 Pro Pro Pro Pro Pro Pro  
 1 5

18

<210> 88  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Pro(CCA)x6

<400> 88

Pro Pro Pro Pro Pro Pro  
 1 5

<210> 89  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Ser(AGC)x6

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 89  
 agc agc agc agc agc agc  
 Ser Ser Ser Ser Ser Ser  
 1 5

18

<210> 90  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Ser(AGC)x6

<400> 90

Ser Ser Ser Ser Ser Ser  
1 5

<210> 91  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ser(TCT)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 91  
tct tct tct tct tct tct  
Ser Ser Ser Ser Ser Ser  
1 5

18

<210> 92  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ser(TCT)x6

<400> 92

Ser Ser Ser Ser Ser Ser  
1 5

<210> 93  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ser(AGT)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 93  
agt agt agt agt agt agt  
Ser Ser Ser Ser Ser Ser  
1 5

18

<210> 94  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Ser(AGT)x6

<400> 94

Ser Ser Ser Ser Ser Ser  
1 5

<210> 95

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ser(TCG)x6

<220>

<221> CDS

<222> (1)..(18)

<400> 95

tcg tcg tcg tcg tcg tcg  
Ser Ser Ser Ser Ser Ser  
1 5

18

<210> 96

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Ser(TCG)x6

<400> 96

Ser Ser Ser Ser Ser Ser  
1 5

<210> 97

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ser(TCA)x6

<220>

<221> CDS

<222> (1)..(18)

<400> 97

tca tca tca tca tca tca  
Ser Ser Ser Ser Ser Ser  
1 5

18

<210> 98

<211> 6

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ser(TCA)x6

<400> 98

Ser Ser Ser Ser Ser Ser  
1 5

<210> 99  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ser(TCC)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 99  
tcc tcc tcc tcc tcc tcc  
Ser Ser Ser Ser Ser Ser  
1 5

18

<210> 100  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Ser(TCC)x6

<400> 100

Ser Ser Ser Ser Ser Ser  
1 5

<210> 101  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Thr(ACA)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 101  
aca aca aca aca aca aca  
Thr Thr Thr Thr Thr Thr  
1 5

18

<210> 102  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Thr(ACA)x6

<400> 102

Thr Thr Thr Thr Thr Thr  
1 5

<210> 103  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Thr(ACG)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 103  
acg acg acg acg acg acg  
Thr Thr Thr Thr Thr Thr  
1 5

18

<210> 104  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Thr(ACG)x6

<400> 104

Thr Thr Thr Thr Thr Thr  
1 5

<210> 105  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Thr(ACT)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 105  
act act act act act act  
Thr Thr Thr Thr Thr Thr  
1 5

18

<210> 106  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Thr(ACT)x6

<400> 106

Thr Thr Thr Thr Thr Thr  
1 5

<210> 107  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Thr(ACC)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 107  
acc acc acc acc acc acc  
Thr Thr Thr Thr Thr Thr  
1 5

18

<210> 108  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Thr(ACC)x6

<400> 108

Thr Thr Thr Thr Thr Thr  
1 5

<210> 109  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Tyr(TAC)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 109  
tac tac tac tac tac tac  
Tyr Tyr Tyr Tyr Tyr Tyr  
1 5

18

<210> 110  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tyr(TAC)x6

<400> 110

Tyr Tyr Tyr Tyr Tyr Tyr  
1 5

<210> 111  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Tyr(TAT)x6

<220>  
<221> CDS  
<222> (1)..(18)

<400> 111  
tat tat tat tat tat tat  
Tyr Tyr Tyr Tyr Tyr Tyr  
1 5

18

<210> 112  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tyr(TAT)x6

<400> 112

Tyr Tyr Tyr Tyr Tyr Tyr  
1 5

<210> 113  
<211> 18  
<212> DNA  
<213> Artificial Sequence



&lt;220&gt;

&lt;223&gt; Val (GTG)x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(18)

&lt;400&gt; 113

gtg gtg gtg gtg gtg gtg

18

Val Val Val Val Val Val

1

5

&lt;210&gt; 114

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Val (GTG)x6

&lt;400&gt; 114

Val Val Val Val Val Val

1

5

&lt;210&gt; 115

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Val (GTT)x6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(18)

&lt;400&gt; 115

gtt gtt gtt gtt gtt gtt

18

Val Val Val Val Val Val

1

5

&lt;210&gt; 116

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Val (GTT)x6

&lt;400&gt; 116

Val Val Val Val Val Val

1

5

&lt;210&gt; 117

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Val (GTC)x6

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 117  
 gtc gtc gtc gtc gtc gtc  
 Val Val Val Val Val Val  
 1 5

18

<210> 118  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Val (GTC)x6

<400> 118

Val Val Val Val Val Val  
 1 5

<210> 119  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Val (GTA)x6

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 119  
 gta gta gta gta gta gta  
 Val Val Val Val Val Val  
 1 5

18

<210> 120  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Val (GTA)x6

<400> 120

Val Val Val Val Val Val

1

5

<210> 121  
 <211> 2583  
 <212> DNA  
 <213> Mouse

<220>  
 <221> CDS  
 <222> (1) .. (2166)

<400> 121  
 gaa ctt cgg gac gag caa act ccg ggc cac agg aag aac cca tcg aac 48  
 Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn  
 1 5 10 15

caa agc agc tta gaa tct gac tcc aat tac ccc tcc att tcc act tcc 96  
 Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser  
 20 25 30

gaa atc gga gac act gag gat gcc ctt cag cag gtg gag gag att ggc 144  
 Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly  
 35 40 45

ata gag aag gca gcc atg gac atg acc gtc ttc ctg aag ctg cag aag 192  
 Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys  
 50 55 60

aga gtg cgc gaa ctt gag cag gag agg aag aag ctg cag gcg cag cta 240  
 Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu  
 65 70 75 80

gaa aag gga cag cag gac agc aag aaa ggg cag gta gaa caa cag aac 288  
 Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn  
 85 90 95

aat ggc tta gat gtg gac cag gac gca gat ata gcc tac aat agt ctg 336  
 Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu  
 100 105 110

aag aga cag gag ctt gag tca gag aac aag aag ctg aag aat gac ctg 384  
 Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu  
 115 120 125

aat gag ctg agg aac ggt gtc gct gac caa gcc atg cag gat aac tcc 432  
 Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser  
 130 135 140

acc cac agc tcc cca gac agc tac agc ctc cta ctg aac cag ctc aag 480  
 Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Leu Asn Gln Leu Lys  
 145 150 155 160

ctg gcc aat gag gag ctc gag gtc cgc aaa gag gag gcg ctg atc ctc 528  
 Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu  
 165 170 175

agg acc cag atc atg aat gcc gac cag cgc cgc ctg tct ggc aag aac 576  
 Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn  
 180 185 190

atg gag ccg aac atc aat gcc aga aca agt tgg ccc aac agt gag aag Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys 195 200 205	624
cac gtg gac cag gaa gac gcc att gag gcc tat cac ggg gtc tgc cag His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln 210 215 220	672
aca aac agg ttg ctg gag gcc cag ctg cag gcc cag agc ctg gag cat Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His 225 230 235 240	720
gag gag gag gtg gaa cat ctc aag gcc cag gtg gaa gcc ctg aaa gag Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu 245 250 255	768
gag atg gac aaa cag cag cag acc ttc tgc cag acc ctg ctg ctc tcc Glu Met Asp Lys Gln Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser 260 265 270	816
cca gag gcc cag gta gaa ttt ggt gtc cag cag gag ata tcc cgg ctg Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu 275 280 285	864
acc aat gag aac ctg gat ttt aag gaa ttg gtg gaa aag ctg gag aag Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys 290 295 300	912
aat gag agg aag ctg aag aag cag ctg aag att tac atg aag aag gtc Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val 305 310 315 320	960
cag gac tta gaa gct gcc cag gcg ttg gca cag agt gac agg agg cac Gln Asp Leu Glu Ala Ala Gln Ala Leu Gln Ser Asp Arg Arg His 325 330 335	1008
cat gaa ctc aca aga cag gtc aca gtc caa cga aaa gag aag gac ttc His Glu Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe 340 345 350	1056
caa ggc atg ctg gag tac cac aaa gag gtc gaa gcc ctc ctc atc cgg Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg 355 360 365	1104
aac ctg gtg aca gac ctg aag cct cag atg ctg ctg ggc acc gtg ccc Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro 370 375 380	1152
tgt ctg cct gca tac ata ctc tat atg tgc atc agg cac gcg gat tac Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr 385 390 395 400	1200
acc aac gat gac ctc aag gtg cac tcg ttg ctg agc tcc acc atc aac Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn 405 410 415	1248
ggc att aag aaa gtc ctc aag aag cac aat gac gac ttt gag atg acg Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr 420 425 430	1296
tca ttc tgg tta tcc aac acc tgc cgc ttc ctt cac tgt ctg aag caa Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln	1344

435	440	445	
tac agt ggt gat gag ggt ttc atg aca cag aac atc gcg aag cag aat Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn 450 455 460			1392
gag cac tgt ctc aag aac ttt gac ctc act gaa tac cgc cag gta cta Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu 465 470 475 480			1440
agc gac ctt tcc att cag atc tat cag cag ctc att aaa atg ccc gag Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu 485 490 495			1488
ggc ttg cta cag cct atg ata gtt tct gcc atg ttg gaa aat gag agt Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser 500 505 510			1536
atc cag ggg ctg tct ggt gtg aga cca act ggt tac cgg aag cgc tcc Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser 515 520 525			1584
tcc agc atg gtg gat gga gag aat tct ttc cat aca gtc ctg tgt gac Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp 530 535 540			1632
cag ggc ctg gac ccc gag att atc ctg cag gtg ttc aaa cag ctc ttc Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe 545 550 555 560			1680
tac atg atc aat gct gtg act ctt aac aac cta ctc ctg cgg aaa gac Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp 565 570 575			1728
gcc tgc tcc tgg agc aca ggc atg caa ctc agg tac aac ata agt caa Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln 580 585 590			1776
ctg gaa gag tgg ctt cgg ggc aaa aac ctt cac cag agt gga gca gtt Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val 595 600 605			1824
cag acc atg gag ccc ctg atc cag gca gcc cag ctc ctc cag ctg aag Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys 610 615 620			1872
aag aaa acc cac gag gat gct gag gcc atc tgc tct ctg tgc acc tcc Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser 625 630 635 640			1920
ctc agc acc cag cag att gtc aaa att tta aac ctc tac act ccc ttg Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu 645 650 655			1968
aat gaa ttt gag gaa cgg gtc aca gtg tcc ttc atc aga aca atc cag Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln 660 665 670			2016
gct cag cta caa gag agg aat gac cct cag cag ctc ctg ctg gac tcc Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser 675 680 685			2064

aag cac gtg ttc cca gtt ctg ttt cca tat aac cca tct gct ctg acc 2112  
 Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr  
 690 695 700

atg gac tcg atc cac atc ccg gcc tgt ctc aac ctg gag ttt ctc aat 2160  
 Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn  
 705 710 715 720

gaa gtc tgaggatgcg tgtttccgag gcgagcgaga aggaagcatg tgctgtcagc 2216  
 Glu Val

cgagagaatg ctaggtgtgt taaatattcc agcgtagatc aaaccatggt agagactggc 2276

gggacgacag aactaaacag cgggggtgcac agttgtcgcc aatgctgctc agaaaacacc 2336

cggaagtgga tttgttaaag ctgtgctttc aggttaaacc aagacacgtc agaacgaaca 2396

gccactctgc agctccagtc gccatataaa aatgccagtt ctacagagtg gaagtgccta 2456

gctttgatct ttgtatatat cttgagaatg ttcaaactga gataatatta aaaacacatg 2516

acgtaaattg cctttgtggg tctttcaaga aatgatggga ctaataacca taagattgac 2576

aggaatt 2583

<210> 122

<211> 722

<212> PRT

<213> Mouse

<400> 122

Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn  
 1 5 10 15

Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser  
 20 25 30

Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly  
 35 40 45

Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys  
 50 55 60

Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu  
 65 70 75 80

Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn  
 85 90 95

Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu  
 100 105 110

Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu  
 115 120 125

Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser  
 130 135 140

Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Leu Asn Gln Leu Lys  
 145 150 155 160

Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu  
 165 170 175

Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn  
 180 185 190

Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys  
 195 200 205

His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln  
 210 215 220

Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His  
 225 230 235 240

Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu  
 245 250 255

Glu Met Asp Lys Gln Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser  
 260 265 270

Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu  
 275 280 285

Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys  
 290 295 300

Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val  
 305 310 315 320

Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala Gln Ser Asp Arg Arg His  
 325 330 335

His Glu Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe  
 340 345 350

Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg  
 355 360 365

Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro  
 370 375 380

Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr  
 385 390 395 400

Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn  
 405 410 415

Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr  
 420 425 430

Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln  
 435 440 445

Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn  
 450 455 460

Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu  
 465 470 475 480

Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu  
 485 490 495

Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser  
 500 505 510

Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser  
 515 520 525

Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp  
 530 535 540

Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe  
 545 550 555 560

Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp  
 565 570 575

Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln  
 580 585 590

Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val  
 595 600 605



Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys  
 610 615 620

Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser  
 625 630 635 640

Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu  
 645 650 655

Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln  
 660 665 670

Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser  
 675 680 685

Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr  
 690 695 700

Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn  
 705 710 715 720

Glu Val

<210> 123  
 <211> 549  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> BAR gene

<220>  
 <221> CDS  
 <222> (1)..(549)

<400> 123  
 agc cca gaa cga cgc ccg gcc gac atc cgc cgt gcc acc gag gcg gac 48  
 Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp  
 1 5 10 15  
 atg ccg gcg gtc tgc acc atc gtc aac cac tac atc gag aca agc acg 96  
 Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr  
 20 25 30  
 gtc aac ttc cgt acc gag ccg cag gaa ccg cag gag tgg acg gac gac 144  
 Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp  
 35 40 45  
 ctc gtc cgt ctg cgg gag cgc tat ccc tgg ctc gtc gcc gag gtg gac 192  
 Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp  
 50 55 60

ggc gag gtc gcc ggc atc gcc tac gcg ggc ccc tgg aag gca cgc aac 240  
 Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn  
 65 70 75 80

gcc tac gac tgg acg gcc gag tcg acc gtg tac gtc tcc ccc cgc cac 288  
 Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His  
 85 90 95

cag cgg acg gga ctg ggc tcc acg ctc tac acc cac ctg ctg aag tcc 336  
 Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser  
 100 105 110

ctg gag gca cag ggc ttc aag agc gtg gtc gct gtc atc ggg ctg ccc 384  
 Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro  
 115 120 125

aac gac ccg agc gtg cgc atg cac gag gcg ctc gga tat gcc ccc cgc 432  
 Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg  
 130 135 140

ggc atg ctg cgg gcg gcc ggc ttc aag cac ggg aac tgg cat gac gtg 480  
 Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val  
 145 150 155 160

ggt ttc tgg cag ctg gac ttc agc ctg ccg gtg ccg ccc cgt ccg gtc 528  
 Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val  
 165 170 175

ctg ccc gtc acc gaa atc tga 549  
 Leu Pro Val Thr Glu Ile  
 180

<210> 124  
 <211> 182  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> BAR gene

<400> 124

Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp  
 1 5 10 15

Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr  
 20 25 30

Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp  
 35 40 45

Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp  
 50 55 60

Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn  
 65 70 75 80

Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His  
                             85                            90                            95

Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser  
                             100                            105                            110

Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro  
                             115                            120                            125

Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg  
                             130                            135                            140

Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val  
                             145                            150                            155                            160

Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val  
                             165                            170                            175

Leu Pro Val Thr Glu Ile  
                             180

<210> 125  
 <211> 366  
 <212> DNA  
 <213> Human

<220>  
 <221> CDS  
 <222> (1) .. (363)

<400> 125  
 atg gga aaa ggt gtg aaa tcc ccg ggg gag aag tca cgc tat gag acc 48  
 Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr  
 1                            5                            10                            15  
 tca ctg aat ctg acc acc aag cgc ttc ctg gag ctg ctg agc cac tcg 96  
 Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser  
                             20                            25                            30  
 gct gac ggt gtc gtc gac ctg aac tgg gct gcc gag gtg ctg aag gtg 144  
 Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val  
                             35                            40                            45  
 cag aag cgg cgc atc tat gac atc acc aac gtc ctt gag ggc atc cag 192  
 Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln  
                             50                            55                            60  
 ctc att gcc aag aag tcc aag aac cac atc cag tgg ctg ggc agc cac 240  
 Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His  
 65                            70                            75                            80  
 acc aca gtg ggc gtc ggc gga cgg ctt gag ggg ttg acc cag gac ctc 288  
 Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu

	85	90	95	
cga cag ctg cag gag agc gag cag cag ctg gac cac ctg atg aat atc				336
Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile	100	105	110	
tgt act acg cag ctg cgc ctg ctc tcc tga				366
Cys Thr Thr Gln Leu Arg Leu Leu Ser	115	120		
<210> 126				
<211> 121				
<212> PRT				
<213> Human				
<400> 126				
Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr	1	5	10	15
Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser	20	25	30	
Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val	35	40	45	
Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln	50	55	60	
Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His	65	70	75	80
Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu	85	90	95	
Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile	100	105	110	
Cys Thr Thr Gln Leu Arg Leu Leu Ser	115	120		